

Ji-Gang Zhang

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

20
papers

473
citations

11
h-index

20
g-index

20
ext. papers

566
ext. citations

3.9
avg, IF

3.1
L-index

#	Paper	IF	Citations
20	Multistage genome-wide association meta-analyses identified two new loci for bone mineral density. <i>Human Molecular Genetics</i> , 2014 , 23, 1923-33	5.6	113
19	Comparative studies of copy number variation detection methods for next-generation sequencing technologies. <i>PLoS ONE</i> , 2013 , 8, e59128	3.7	112
18	Replication of 6 obesity genes in a meta-analysis of genome-wide association studies from diverse ancestries. <i>PLoS ONE</i> , 2014 , 9, e96149	3.7	45
17	CNV-TV: a robust method to discover copy number variation from short sequencing reads. <i>BMC Bioinformatics</i> , 2013 , 14, 150	3.6	31
16	Metabolomic profiles associated with bone mineral density in US Caucasian women. <i>Nutrition and Metabolism</i> , 2018 , 15, 57	4.6	30
15	Network-based proteomic analysis for postmenopausal osteoporosis in Caucasian females. <i>Proteomics</i> , 2016 , 16, 12-28	4.8	28
14	Attenuated monocyte apoptosis, a new mechanism for osteoporosis suggested by a transcriptome-wide expression study of monocytes. <i>PLoS ONE</i> , 2015 , 10, e0116792	3.7	19
13	Is GSN significant for hip BMD in female Caucasians?. <i>Bone</i> , 2014 , 63, 69-75	4.7	16
12	Quantitative proteomics and integrative network analysis identified novel genes and pathways related to osteoporosis. <i>Journal of Proteomics</i> , 2016 , 142, 45-52	3.9	16
11	Low-, high-coverage, and two-stage DNA sequencing in the design of the genetic association study. <i>Genetic Epidemiology</i> , 2017 , 41, 187-197	2.6	15
10	Genome-wide Survey of Runs of Homozygosity Identifies Recessive Loci for Bone Mineral Density in Caucasian and Chinese Populations. <i>Journal of Bone and Mineral Research</i> , 2015 , 30, 2119-26	6.3	11
9	Multivariate analysis of genomics data to identify potential pleiotropic genes for type 2 diabetes, obesity and dyslipidemia using Meta-CCA and gene-based approach. <i>PLoS ONE</i> , 2018 , 13, e0201173	3.7	8
8	MicroRNA-miRNA interaction analysis to detect potential dysregulation in complex diseases. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015 , 4, 1	1.6	7
7	Integrative analysis of GWASs, human protein interaction, and gene expression identified gene modules associated with BMDs. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014 , 99, E2392-9	5.6	7
6	A Statistical Test for Differential Network Analysis Based on Inference of Gaussian Graphical Model. <i>Scientific Reports</i> , 2019 , 9, 10863	4.9	5
5	Genetic risk factors identified in populations of European descent do not improve the prediction of osteoporotic fracture and bone mineral density in Chinese populations. <i>Scientific Reports</i> , 2019 , 9, 6086	4.9	4
4	Mass spectrometry based proteomics profiling of human monocytes. <i>Protein and Cell</i> , 2017 , 8, 123-133	7.2	3

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| 3 | Detection of common copy number variation with application to population clustering from next generation sequencing data. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference, 2012, 2012, 1246-9</i> | 0.9 | 2 |
| 2 | Fusing Gene Interaction to Improve Disease Discrimination on Classification Analysis. <i>Advancements in Genetic Engineering, 2012, 1, 1000102</i> | | 1 |
| 1 | Population clustering based on copy number variations detected from next generation sequencing data. <i>Journal of Bioinformatics and Computational Biology, 2014, 12, 1450021</i> | 1 | |